Figure 1

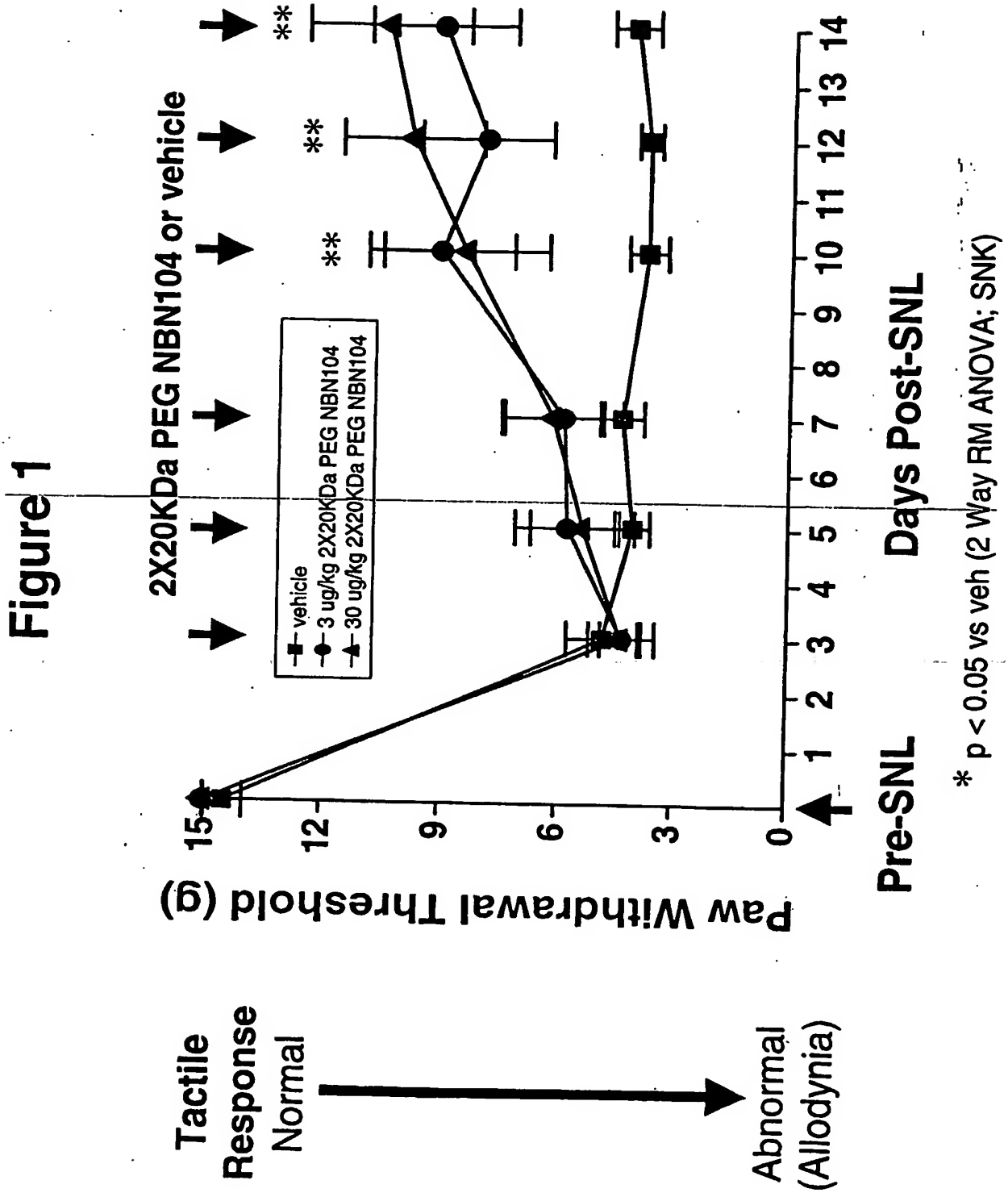

2X20KDa PEG NBN104 or vehicle
vehicle
3 ug/kg 2X20KDa PEG NBN104
30 ug/kg 2X20KDa PEG NBN104
**
**
**
Paw Withdrawal Threshold (g)
15
12
9
6
3
0
1 2 3 4 5 6 7 8 9 10 11 12 13 14
Pre-SNL
Days Post-SNL
Tactile Response
Normal
Abnormal (Allodynia)
* p < 0.05 vs veh (2 Way RM ANOVA; SNK)

Figure 2

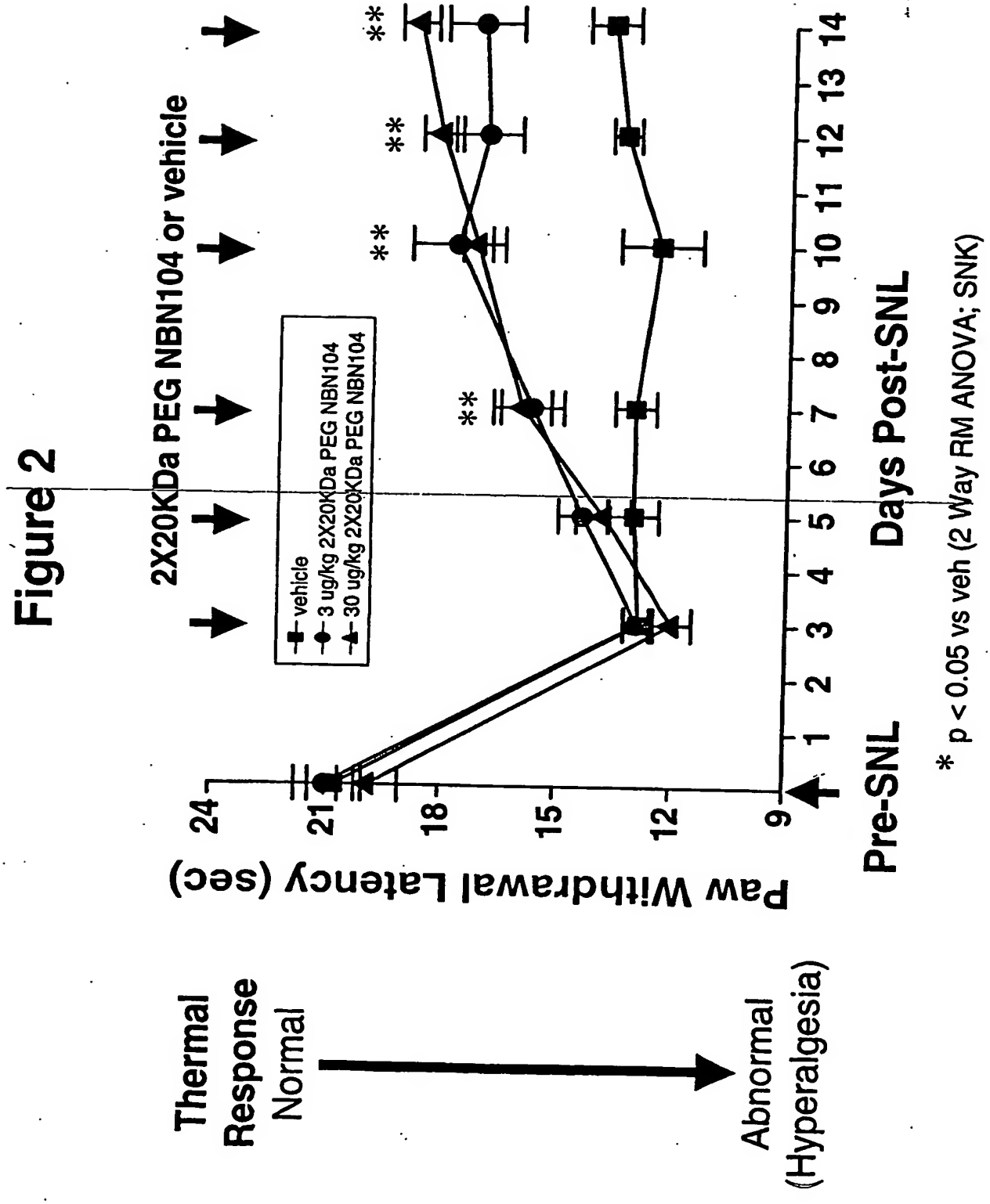

2X20KDa PEG NBN104 or vehicle
vehicle
3 ug/kg 2X20KDa PEG NBN104
30 ug/kg 2X20KDa PEG NBN104
Paw Withdrawal Latency (sec)
24
21
18
15
12
9
Pre-SNL
1 2 3 4 5 6 7 8 9 10 11 12 13 14
Days Post-SNL
Thermal Response
Normal
Abnormal (Hyperalgesia)
** p < 0.05 vs veh (2 Way RM ANOVA; SNK)

FIG. 3

```
1     AGGPGSRARAAGARGCRLRSQLVPVRALGLGHRSDELVRF   human
      AGTRSSRARTTDARGCRLRSQLVPVSALGLGHSSDELIRF   mouse
      AGTRSSRARATDARGCRLRSQLVPVSALGLGHSSDELIRF   rat
      ||   ||||   |||||||||||||| |||||| |||| ||
      ag---srar---argcrlrsqlvpv-alglgh-sdel-rf   consensus

41    RFCSGSCRRARSPHDLSLASLLGAGALRPPPGSRPVSQPC   human
      RFCSGSCRRARSQHDLSLASLLGAGALRSPPGSRPISQPC   mouse
      RFCSGSCRRARSPHDLSLASLLGAGALRSPPGSRPISQPC   rat
      ||||||||||||||||||||||||||||||||||||||||
      rfcsgscrrars-hdlslasllgagalr-ppgsrp-sqpc   consensus

81    CRPTRYEAVSFMDVNSTWRTVDRLSATACGCLG          human (SEQ ID NO:2)
      CRPTRYEAVSFMDVNSTWRTVDHLSATACGCLG          mouse (SEQ ID NO:3)
      CRPTRYEAVSFMDVNSTWRTVDHLSATACGCLG          rat   (SEQ ID NO:4)
      |||||||||||||||||||| ||||||||||
      crptryeavsfmdvnstwrtvd-lsatacgclg          consensus (SEQ ID NO:1)
                    *                              * = Asn95
```

FIG. 4

Consensus sequence: (SEQ ID NO:1)

Ala Gly Xaa1 Xaa2 Xaa3 Ser Arg Ala Arg Xaa4 Xaa5 Xaa6 Ala Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Xaa7 Ala Leu Gly Leu Gly His Xaa8 Ser Asp Glu Leu Xaa9 Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Xaa10 His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Xaa11 Pro Pro Gly Ser Arg Pro Xaa12 Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Xaa13 Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly

wherein:

Xaa_1 is Gly or Thr	Xaa_6 is Gly or Asp	Xaa_{11} is Pro or Ser
Xaa_2 is Pro or Arg	Xaa_7 is Arg or Ser	Xaa_{12} is Val or Ile
Xaa_3 is Gly or Ser	Xaa_8 is Arg or Ser	Xaa_{13} is Arg or His
Xaa_4 is Ala or Thr	Xaa_9 is Val or Ile	
Xaa_5 is Ala or Thr	Xaa_{10} is Pro or Gln	

FIG. 5

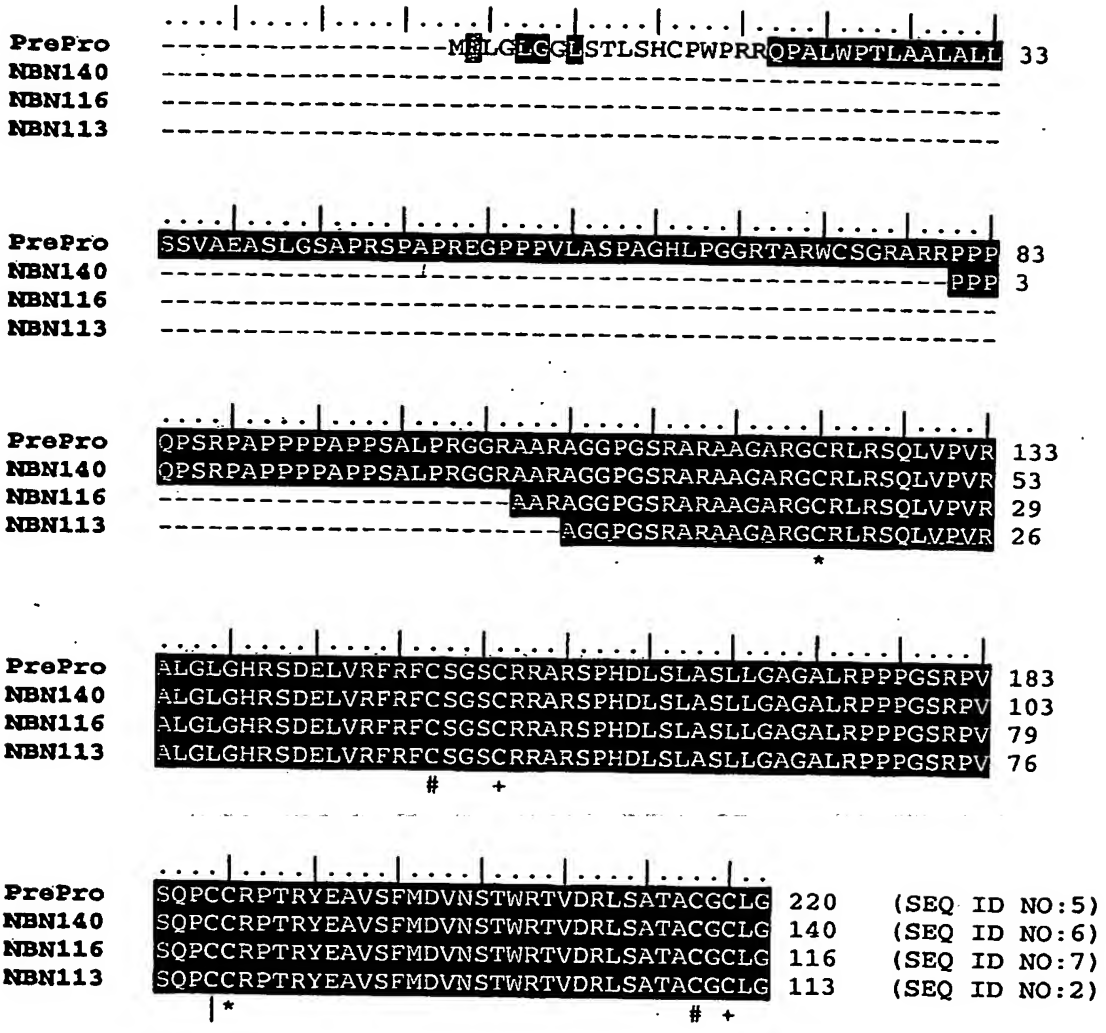
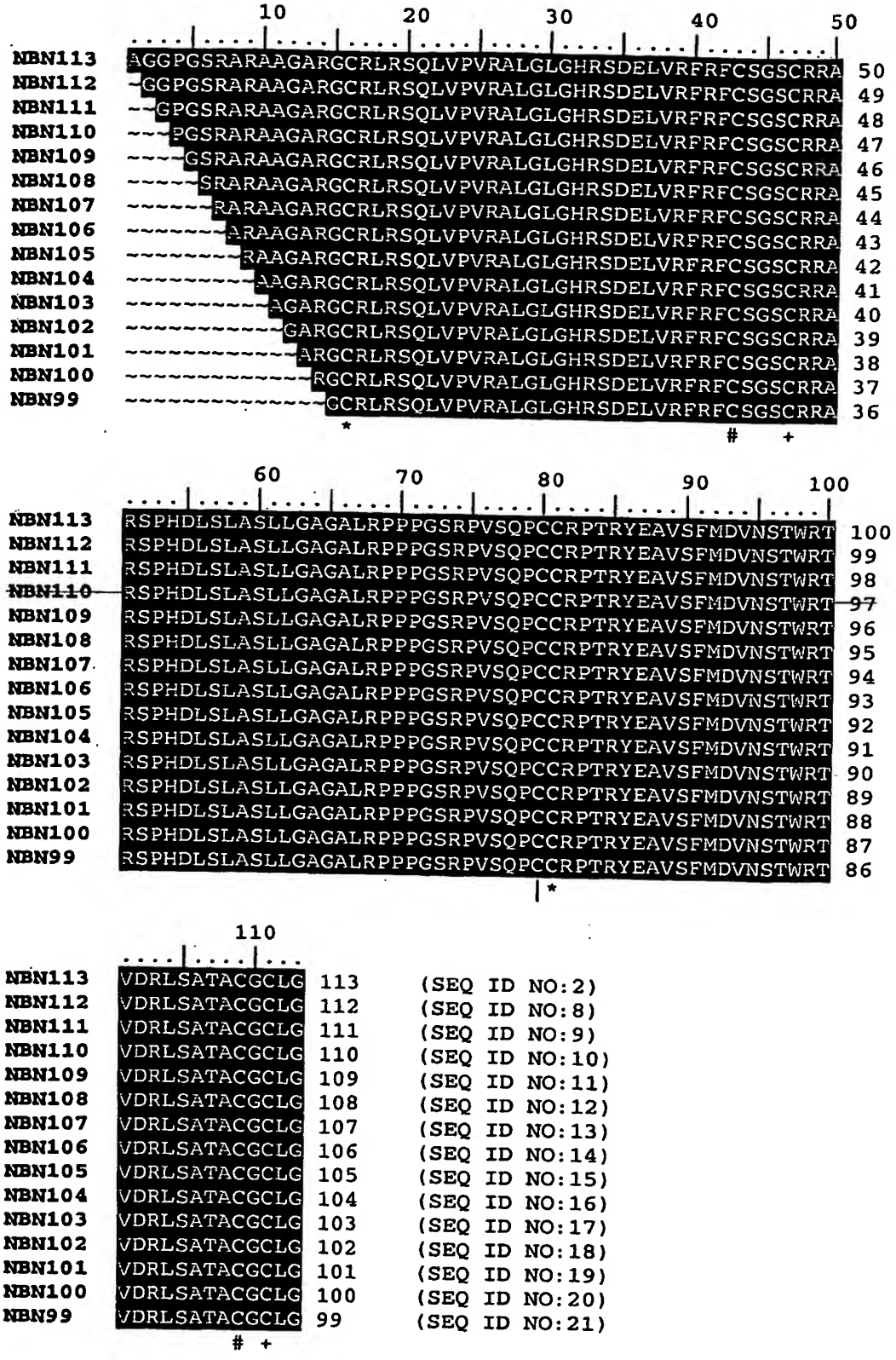

PrePro
NBN140
NBN116
NBN113
33
83
3
133
53
29
26
183
103
79
76
220
140
116
113
(SEQ ID NO:5)
(SEQ ID NO:6)
(SEQ ID NO:7)
(SEQ ID NO:2)

FIG. 6


10 20 30 40 50
NBN113 AGGPGSRARAAGARGCRLRSQLVPVRALGLGHRSDELVRFRFCSGSCRRA 50
NBN112 -GGPGSRARAAGARGCRLRSQLVPVRALGLGHRSDELVRFRFCSGSCRRA 49
NBN111 --GPGSRARAAGARGCRLRSQLVPVRALGLGHRSDELVRFRFCSGSCRRA 48
NBN110 ---PGSRARAAGARGCRLRSQLVPVRALGLGHRSDELVRFRFCSGSCRRA 47
NBN109 ----GSRARAAGARGCRLRSQLVPVRALGLGHRSDELVRFRFCSGSCRRA 46
NBN108 -----SRARAAGARGCRLRSQLVPVRALGLGHRSDELVRFRFCSGSCRRA 45
NBN107 ------RARAAGARGCRLRSQLVPVRALGLGHRSDELVRFRFCSGSCRRA 44
NBN106 -------ARAAGARGCRLRSQLVPVRALGLGHRSDELVRFRFCSGSCRRA 43
NBN105 --------RAAGARGCRLRSQLVPVRALGLGHRSDELVRFRFCSGSCRRA 42
NBN104 ---------AAGARGCRLRSQLVPVRALGLGHRSDELVRFRFCSGSCRRA 41
NBN103 ----------AGARGCRLRSQLVPVRALGLGHRSDELVRFRFCSGSCRRA 40
NBN102 -----------GARGCRLRSQLVPVRALGLGHRSDELVRFRFCSGSCRRA 39
NBN101 ------------ARGCRLRSQLVPVRALGLGHRSDELVRFRFCSGSCRRA 38
NBN100 -------------RGCRLRSQLVPVRALGLGHRSDELVRFRFCSGSCRRA 37
NBN99 --------------GCRLRSQLVPVRALGLGHRSDELVRFRFCSGSCRRA 36
60 70 80 90 100
NBN113 RSPHDLSLASLLGAGALRPPPGSRPVSQPCCRPTRYEAVSFMDVNSTWRT 100
NBN112 RSPHDLSLASLLGAGALRPPPGSRPVSQPCCRPTRYEAVSFMDVNSTWRT 99
NBN111 RSPHDLSLASLLGAGALRPPPGSRPVSQPCCRPTRYEAVSFMDVNSTWRT 98
NBN110 RSPHDLSLASLLGAGALRPPPGSRPVSQPCCRPTRYEAVSFMDVNSTWRT 97
NBN109 RSPHDLSLASLLGAGALRPPPGSRPVSQPCCRPTRYEAVSFMDVNSTWRT 96
NBN108 RSPHDLSLASLLGAGALRPPPGSRPVSQPCCRPTRYEAVSFMDVNSTWRT 95
NBN107 RSPHDLSLASLLGAGALRPPPGSRPVSQPCCRPTRYEAVSFMDVNSTWRT 94
NBN106 RSPHDLSLASLLGAGALRPPPGSRPVSQPCCRPTRYEAVSFMDVNSTWRT 93
NBN105 RSPHDLSLASLLGAGALRPPPGSRPVSQPCCRPTRYEAVSFMDVNSTWRT 92
NBN104 RSPHDLSLASLLGAGALRPPPGSRPVSQPCCRPTRYEAVSFMDVNSTWRT 91
NBN103 RSPHDLSLASLLGAGALRPPPGSRPVSQPCCRPTRYEAVSFMDVNSTWRT 90
NBN102 RSPHDLSLASLLGAGALRPPPGSRPVSQPCCRPTRYEAVSFMDVNSTWRT 89
NBN101 RSPHDLSLASLLGAGALRPPPGSRPVSQPCCRPTRYEAVSFMDVNSTWRT 88
NBN100 RSPHDLSLASLLGAGALRPPPGSRPVSQPCCRPTRYEAVSFMDVNSTWRT 87
NBN99 RSPHDLSLASLLGAGALRPPPGSRPVSQPCCRPTRYEAVSFMDVNSTWRT 86
110
NBN113 VDRLSATACGCLG 113 (SEQ ID NO:2)
NBN112 VDRLSATACGCLG 112 (SEQ ID NO:8)
NBN111 VDRLSATACGCLG 111 (SEQ ID NO:9)
NBN110 VDRLSATACGCLG 110 (SEQ ID NO:10)
NBN109 VDRLSATACGCLG 109 (SEQ ID NO:11)
NBN108 VDRLSATACGCLG 108 (SEQ ID NO:12)
NBN107 VDRLSATACGCLG 107 (SEQ ID NO:13)
NBN106 VDRLSATACGCLG 106 (SEQ ID NO:14)
NBN105 VDRLSATACGCLG 105 (SEQ ID NO:15)
NBN104 VDRLSATACGCLG 104 (SEQ ID NO:16)
NBN103 VDRLSATACGCLG 103 (SEQ ID NO:17)
NBN102 VDRLSATACGCLG 102 (SEQ ID NO:18)
NBN101 VDRLSATACGCLG 101 (SEQ ID NO:19)
NBN100 VDRLSATACGCLG 100 (SEQ ID NO:20)
NBN99 VDRLSATACGCLG 99 (SEQ ID NO:21)